AMENDMENTS TO THE CLAIMS

Please amend claims 1, 9, 10, 12 and 17 as provided below in the Listing of Claims.

Please cancel claims 3, 4, 7, 8, 11, 14, 15, 18, 20 and 21.

Please add claims 23-27.

The listing of claims will replace all prior version, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for identifying loss of imprinting (LOI) of the IGF2 gene in a human subject with colorectal cancer, comprising analyzing a biological sample from the subject for hypomethylation of a differentially methylated region (DMR) of ~~at least one of the H19 gene and~~ the IGF2 gene, wherein the biological sample is a blood sample or a colon mucosa sample; and

detecting hypomethylation of the DMR in the subject, wherein hypomethylation is as compared to the half-methylation of the normally imprinted gene, and wherein further the DMR of the IGF2 gene comprises SEQ ID NO:1, wherein detection of hypomethylation of the DMR in the subject correlates with loss of imprinting (LOI).

Claims 2-8. (Canceled)

9. (Currently amended) The method of claim 1, wherein the analysis is performed by contacting the biological sample with a primer pair comprising ~~at least one pair of:~~

SEQ ID NO:2 and SEQ ID NO:3~~;~~

~~SEQ ID NO:4 and SEQ ID NO:5;~~

~~SEQ ID NO:27 and SEQ ID NO:28; and~~

~~SEQ ID NO:29 and SEQ ID NO:30~~.

10. (Currently amended) A method for identifying an increased risk of developing colorectal cancer in a human subject, comprising analyzing a biological sample from the subject for hypomethylation of a differentially methylated region (DMR) of an ~~H19 gene or an~~ IGF2 gene, wherein hypomethylation is as compared to the half-methylation of the normally imprinted gene, and wherein further the DMR of the IGF2 gene comprises SEQ ID NO:1, wherein detection of hypomethylation of the DMR in the subject correlates with loss of imprinting (LOI), ~~and~~ wherein LOI is indicative of increased risk of the subject developing colorectal cancer, and wherein the biological sample is a blood sample or a colon mucosa sample.

11. (Canceled)

12. (Currently amended) The method of claim 10, wherein the method comprises bisulfite genomic sequencing ~~performed using the primer pair SEQ ID NO:23 and SEQ ID NO:24, followed by the primer pair SEQ ID NO:25 and SEQ ID NO:26~~.

13. (Original) The method of claim 10, wherein the subject is not a subject known to have a colorectal neoplasm.

Claims 14-15. (Canceled)

16. (Original) The method of claim 10, wherein the biological sample is a blood sample.

17. (Currently amended) A method for identifying an increased risk of developing colorectal cancer in a human subject, comprising analyzing a first genomic DNA sample from the subject for hypomethylation of a DMR of an IGF2 gene, wherein hypomethylation is as compared to the half-methylation of the normally imprinted gene, and wherein further the DMR of the IGF2 gene comprises SEQ ID NO:1, wherein hypomethylation of the IGF2 gene correlates with the loss of imprinting of the IGF2 gene, ~~and~~ wherein a loss of imprinting of the IGF2 gene is indicative of an increased risk of developing colorectal cancer, and wherein the genomic DNA

sample is from a blood sample or a colon mucosa sample, thereby identifying an increased risk of developing colorectal cancer in the subject.

Claims 18-22. (Canceled)

23. (New) The method of claim 1, wherein the biological sample is a blood sample.

24. (New) The method of claim 1, wherein the biological sample is a colon mucosa sample.

25. (New) The method of claim 10, wherein the biological sample is a colon mucosa sample.

26. (New) The method of claim 17, wherein the genomic DNA sample is from a colon mucosa sample.

27. (New) The method of claim 17, wherein the genomic DNA sample is from a blood sample.